Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-24.   (cancelled)

25. (withdrawn) A method for haplotyping the Interleukin 4 Receptor Alpha (IL4Rα) gene of an individual which comprises determining whether the individual has one or more haplotypes in Table 5.

26. (previously added) A method for predicting a haplotype pair for the Interleukin 4 Receptor Alpha(IL4Rα) gene of an individual comprising:

  (a) identifying an IL4Rα genotype for the individual at each of the polymorphic sites in the haplotype pairs in Table 4, wherein the polymorphic sites consist of PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS10, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS24, PS25, PS26, PS27, PS28, PS29, PS30, PS31, PS32, PS33, PS34, PS35, PS36, PS37, PS38, PS39, PS40, PS41, PS42, PS43, PS44, and PS45;

  (b) enumerating all possible haplotype pairs which are consistent with the genotype;

  (c) accessing data containing the IL4Rα haplotype pairs determined in a reference population, wherein the IL4Rα haplotype pairs comprise the haplotype pairs of table 4; and

  (d) assigning a haplotype pair to the individual that is consistent with the data.

27.   (previously added) The method of claim 26, wherein the assigning step comprises:

  a) comparing each of the possible haplotype pairs to the haplotype pairs in the accessed data; and

  b) using the result of the comparing step to assign a haplotype pair to the individual,

    wherein if the result of the comparing step is that only one of the haplotype pairs in the accessed data matches a possible haplotype pair, then that haplotype pair is assigned to the individual, and

    if the result of the comparing step is that only one haplotype represented in the haplotype pairs in the accessed data is consistent with a possible haplotype pair for an individual, then the individual is assigned a haplotype pair containing this known haplotype and a new haplotype derived by subtracting the known haplotype from the possible haplotype pair.

28.   (previously added) The method of claim 26, wherein the identifying step comprises performing an assay for genotyping at least one of the polymorphic sites, wherein the assay is selected from the group consisting of:

   a)   a primer extension assay;

   b)   an allele-specific PCR assay;

   c)   a nucleic acid amplification assay;

   d)   a hybridization assay;

   e)   a mismatch-detection assay;

   f)   an enzymatic nucleic acid cleaving assay; and

   g)   a sequencing assay.

29.   (previously added) The method of claim 26, wherein the identifying step comprises indirectly determining the genotype of at least one of the polymorphic sites by genotyping a second polymorphic site in linkage disequilibrium with the polymorphic site.

30. (new)   The method of claim 26, wherein the identifying step comprises directly determining the genotype at each of PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS10, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS24, PS25, PS26, PS27, PS28, PS29, PS30, PS31, PS32, PS33, PS34, PS35, PS36, PS37, PS38, PS39, PS40, PS41, PS42, PS43, PS44, and PS45.